

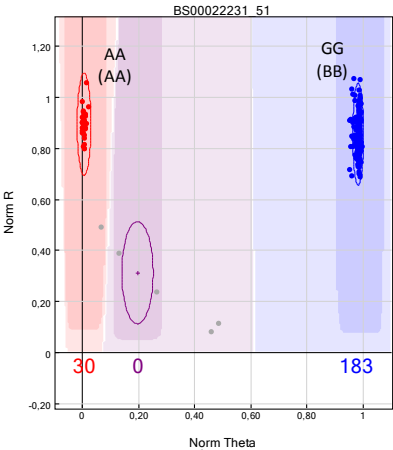
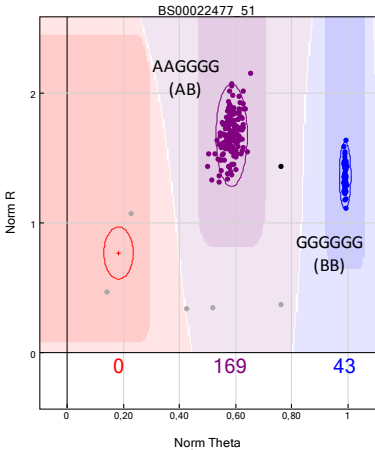
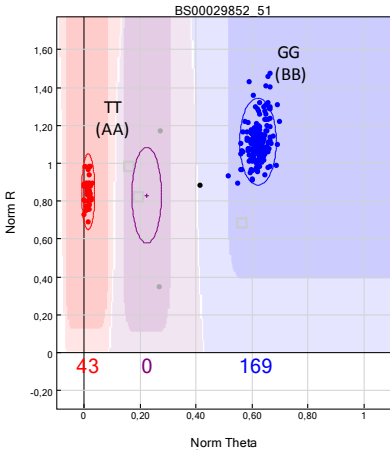
Supplementary Figure S1: SNP calls received from TraitGenetics, cluster plots produced from raw SNP chip data using the software GenomeStudio and comparison with publically available wheat sequence data and Sanger sequencing of regions flanking SNPs in up to six homeologous and paralogous copies of probe targets (5B1, 5B2, 5A1, 5A2, 5D1, 5D2). - indicates no copy detected (BLAST hits were filtered with an E-value threshold of $10e-5$).

Hap-5B-RDMa	GENE-2890 482 probe		Excalibur c25522 755 probe		Kukri c46570 214 probe	
Putative chromosome targets and homeologous/parlogous copies	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)
5B - copy 1, Hap-5B-RDMa-h1	G	100%*	C	100%*	A	100%*
5B - copy 1, Hap-5B-RDMa-h2	A	98%*	T	98%*	G	98%*
5B - copy 2	-	-	C	90,19%+	G	100%+
5A - copy 1	A	96%*	T	96%+	G	98%+
5A - copy 2	-	-	C	96,07%+	-	-
5D - copy 1	A	100%*	C	86%+	G	100%+
5D -copy 2	-	-	C	92,15%+	-	-
SNP type	hemi		hemi		hemi	
Cluster positions from GenomeStudio using standard manifest file (putative nucleotide alleles for called cluster indicated)						

Hap-5B-RDMa	RAC875 c12293 588 probe		RAC875 c18088 2222 probe		BobWhite c43 86 probe	
Putative chromosome targets and homeologous/paralogous copies	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)
5B - copy 1, Hap-5B-RDMa-h1	G	100%*	G	100%* and 98%*	G	100%* and 74%*
5B - copy 1, Hap-5B-RDMa-h2	A	98%*	A	98%*	A	98%*
5B - copy 2	-	-	-	-	-	-
5A- copy 1	G	96%*	G	98%+	A	86%+
5A - copy 2	-	-	-	-	-	-
5D - copy 1	A	98%*	G	98%+	A	56%+
5D -copy 2	-	-	-	-	-	-
SNP type	hemi		hemi		simple	
Cluster positions from GenomeStudio using standard manifest file (putative nucleotide alleles for called cluster indicated)						

Hap-5B-RDMa	RAC875 c18088 950 probe		RAC875 c24226 1356 probe		Excalibur c60554 394 probe	
Putative chromosome targets and homeologous/paralogous copies	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)
5B - copy 1, Hap-5B-RDMa-h1	C	100%*	A	100%*	G	100%*
5B - copy 1, Hap-5B-RDMa-h2	T	100%*	C	100%*	A [†]	100%*
5B - copy 2	-	-	C	82%+	-	-
5A- copy 1	C	100%*	C	98%+	T	100%*
5A - copy 2	-	-	-	-	-	-
5D - copy 1	T	98%*	C	100%+	G	100%*
5D -copy 2	-	-	-	-	-	-
SNP type	hemi		hemi		hemi	
Cluster positions from GenomeStudio using standard manifest file (putative nucleotide alleles for called cluster indicated)						

[†] Sanger sequencing revealed for SNP Excalibur_c60554_394 a A/G polymorphism instead of reported T/G polymorphism called from 90K SNP array

Hap-5B-RDMb	BS00022231 51 probe		BS00022477 51 probe		BS00029852 51 probe	
Putative chromosome targets and homeologous/paralogous copies	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)
5B - copy 1, Hap-5B-RDMb-h1	G	100%*	A	100%*	G	100%*
5B - copy 1, Hap-5B-RDMb-h2	A	100%*	G	100%*	T	100%*
5B - copy 1, Hap-5B-RDMb-h3	G	100%*	G	100%*	T	100%*
5B - copy 1, Hap-5B-RDMb-h8	G	100%*	A	100%*	G	100%*
5A - copy 1	-	-	G	98%*	T	46%+
5D - copy 1	-	-	G	96%*	T	79%+
SNP type	simple		hemi		simple	
Cluster positions from GenomeStudio using standard manifest file (putative nucleotide alleles for called cluster indicated)						

Hap-5B-RDMb	BS00110293 51 probe		IACX6288 probe		Tdurum contig48959 1172 probe	
Putative chromosome targets and homeologous/paralogous copies	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)	SNPs called from alignment to public sequences	Similarity of 50 bp probe with IWGSC reference(+) or sequenced DNA(*)
5B - copy 1, Hap-5B-RDMb-h1	A	100%*	T	94,91%*	G	100%*
5B - copy 1, Hap-5B-RDMb-h2	G	100%*	C	96,6%*	G	100%*
5B - copy 1, Hap-5B-RDMb-h3	G	98%*	C	96,6%*	T	100%*
5B - copy 1, Hap-5B-RDMb-h8	G	98%*	C	97%*	T	100%*
5A - copy 1	-	-	C	100%+	-	-
5D - copy 1	-	-	C	98%+	-	-
SNP type	unclear (densely spaced homozygous subclusters)		hemi		simple	
Cluster positions from GenomeStudio using standard manifest file (putative nucleotide alleles for called cluster indicated)	